AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

1-17.   Canceled.

18.   (Currently amended) A computer-based system ~~incorporating a classification tree model which incorporates Bayesian analysis~~ for ~~the~~ statistical prediction of binary outcomes, said system comprising a processor, an input, an output, and a computer-readable storage medium;

wherein the processor generates a tree model using Bayesian analysis, ~~wherein~~ the tree model ~~comprises~~ comprising one or more nodes representing metagenes predictive of lymph node metastasis, and one or more nodes representing clinical risk factors;

wherein the metagenes are generated by sorting expression data from a plurality of genes into a plurality of clusters and extracting a singular dominant factor from each cluster using singular value decomposition,

wherein the processor generates a predicted disease outcome for a subject using the tree model; and

wherein the predicted disease outcome is displayed on the output.

19.   (Withdrawn) A computer readable medium having computer readable program codes embodied therein for predicting lymph node metastasis in an individual afflicted with breast cancer, the computer readable medium program codes performing functions comprising generating a prediction of lymph node metastasis from the classification tree model of claim 18.

20.   (Withdrawn) The method of claim 19, wherein one of the metagenes is Mg20.

21.   (Withdrawn) A method of predicting lymph node metastasis in an individual afflicted with breast cancer, by combining metagene expression data with clinical risk factors, the method comprising:

(i) obtaining a nucleic sample from a tumor biopsy of the individual and generating an expression profile from the nucleic acid sample of at least two-genes whose expression is correlated with breast cancer recurrent; and

(ii) generating a prediction of lymph node metastasis from the classification tree model of claim 18.

22.   (Withdrawn) The method of claim 21, wherein one of the metagenes is Mg20.

23.   (Withdrawn) The method of claim 21, wherein the clinical risk factors are selected from auxiliary lymph node status, estrogen receptor (ER) status, tumor size and treatment factors.

24.   (Previously presented) The computer-based system of claim 18, wherein said clinical risk factor is selected from lymph node status, patient age, hormone receptor status, tumor size, or a combination thereof.

25.   (Previously presented) The computer-based system of claim 18, wherein said outcome is tumor recurrence.

26.   (New) The computer-based system of claim 18, wherein gene clusters are formed using k-means clustering.

27.   (New) The computer-based system of claim 18, wherein the Bayesian analysis uses sequences of Bayes factor based tests of association to rank and select predictors that define a node split.

28.   (New) The computer-based system of claim 18, wherein the processor generates the tree model using forward generation of at least one class of trees with high marginal likelihood, wherein prediction of said class of trees is conducted using model averaging.

29.   (New) The computer-based system of claim 28, wherein model averaging comprises: generating a weighted prediction of a tree by determining its implied posterior probability by a score; evaluating the score to exclude unlikely trees; evaluating the posterior and predictive

distribution at each node and leaf of a tree; and applying said posterior and predictive

distribution to the evaluation of each tree and averaging predictions across trees for future

predictive cases.